



CGCTCAGGATACGACTTCGCTAGATCGGATCCCGGATATTATATAGCTCGATCGATC  
 TTCTCTATATCGCGGATCGCTATATACACACACACCGCGCGATAGCATGACTGATCTA  
 CCCAATCTTCGCATACGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
 CACAGACTACGCTACCTCCTACTTACTTAACCAATTCGGAGAGCGCCGCGGATCGGAGAG

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1: [AL050320](#). Human DNA sequenc...[gi:7263998]

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LOCUS HSJ1077I2 107057 bp DNA linear PRI 25-OCT-2002  
 DEFINITION Human DNA sequence from clone RP5-1077I2 on chromosome 20. Contains the 3' end of the SPTLC2L gene for serine palmitoyltransferase long chain base subunit 2-like (aminotransferase 2), the 5' end of C20orf82 gene for a novel protein, part of 2 novel genes and a putative CpG island, complete sequence.  
 ACCESSION AL050320  
 VERSION AL050320.19 GI:7263998  
 KEYWORDS HTG; aminotransferase; CpG island; serine palmitoyltransferase; SPTLC2L.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 107057)  
 AUTHORS Smith,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-OCT-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
 COMMENT On Mar 19, 2000 this sequence version replaced gi:6523711. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-1077I2 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
 VECTOR: pCYPAC2  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

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 IMPORTANT: This sequence is not the entire insert of clone RP5-1077I2. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP5-1077I2 is at 107057 in this sequence. The true right end of clone RP4-718P11 is at 100 in this sequence.

FEATURES	Location/Qualifiers
source	1..107057 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="20" /clone="RP5-1077I2" /clone_lib="RPCI-5"
<u>repeat region</u>	complement(64..135) /note="L3b repeat: matches 1389..1462 of consensus"
<u>repeat region</u>	complement(164..264) /note="MIR repeat: matches 54..149 of consensus"
<u>repeat region</u>	complement(274..490) /note="L1PA4 repeat: matches 5942..6155 of consensus"
<u>repeat region</u>	277..290 /note="4.7 copies 3 mer TTA 21% conserved"
<u>gene</u>	730..844 /gene="SPTLC2L"
<u>mRNA</u>	<730..844 /gene="SPTLC2L" /product="dJ1077I2.2 (serine palmitoyltransferase, long chain base subunit 2-like (aminotransferase 2), variant 1)" /note="continued from dJ718P11.1.1 in Em:AL109983 match: ESTs: Em:BQ011413" /evidence=not_experimental
<u>CDS</u>	<730..756 /gene="SPTLC2L" /note="continued from dJ718P11.1.1 in Em:AL109983" /codon_start=1 /evidence=not_experimental /product="dJ1077I2.2 (serine palmitoyltransferase, long chain base subunit 2-like (aminotransferase 2), variant 1)" /protein_id="CAD54807.1" /db_xref="GI:24412822" /db_xref="GOA:Q8IV87" /db_xref="SPTREMBL:Q8IV87" /translation="VICCVMKI"
<u>polyA signal</u>	824..829 /gene="SPTLC2L"
<u>polyA site</u>	844 /gene="SPTLC2L"
<u>repeat region</u>	884..896 /note="2.6 copies 5 mer AAAAT 26% conserved"
<u>repeat region</u>	992..1002 /note="2.2 copies 5 mer TTCTT 22% conserved"
<u>repeat region</u>	1473..1494 /note="11.0 copies 2 mer AC 44% conserved"
<u>repeat region</u>	1569..1580 /note="2.0 copies 6 mer CAAATG 24% conserved"
<u>repeat region</u>	1871..1883 /note="2.2 copies 6 mer TTTTCC 26% conserved"
<u>repeat region</u>	complement(2399..2464) /note="MER5A repeat: matches 41..105 of consensus"
<u>misc feature</u>	2513..2619 /note="match: STS: Em:Z94369"

repeat region 2665..2674  
/note="2.5 copies 4 mer GATG 20% conserved"

repeat region 3122..3136  
/note="3.8 copies 4 mer TCTT 21% conserved"

repeat region 3368..3378  
/note="2.2 copies 5 mer ACAA 22% conserved"

repeat region 3615..3649  
/note="2.7 copies 13 mer TTCATGATTTTAA 70% conserved"

repeat region 3833..3848  
/note="8.0 copies 2 mer CA 23% conserved"

repeat region 3889..3898  
/note="2.5 copies 4 mer TGGT 20% conserved"

repeat region 4108..4247  
/note="MER5A repeat: matches 44..184 of consensus"

repeat region 4367..4377  
/note="2.2 copies 5 mer CTTCT 22% conserved"

misc feature complement(4488..5147)  
/note="match: GSS: Em:AQ262066"

repeat region 4535..4556  
/note="5.5 copies 4 mer TCTT 35% conserved"

repeat region complement(4541..4855)  
/note="AluSp repeat: matches 1..313 of consensus"

repeat region 4554..4570  
/note="17.0 copies 1 mer T 34% conserved"

repeat region 4637..4648  
/note="2.0 copies 6 mer ACCTCC 24% conserved"

repeat region 5056..5066  
/note="3.7 copies 3 mer GAT 22% conserved"

repeat region 5325..5364  
/note="20.0 copies 2 mer TG 44% conserved"

repeat region 5450..5460  
/note="2.8 copies 4 mer AAAT 22% conserved"

repeat region complement(5498..5566)  
/note="LTR16A repeat: matches 382..444 of consensus"

repeat region complement(5567..5760)  
/note="MER63A repeat: matches 1..209 of consensus"

repeat region complement(5761..6016)  
/note="LTR16A repeat: matches 95..382 of consensus"

repeat region complement(6066..6288)  
/note="L1MC5 repeat: matches 7695..7923 of consensus"

misc feature 7638..8163  
/note="match: GSS: Em:B52469"

repeat region 8095..8512  
/note="HAL1 repeat: matches 827..1248 of consensus"

repeat region 8095..8108  
/note="2.3 copies 6 mer AATAGA 28% conserved"

repeat region 8328..8341  
/note="2.0 copies 7 mer TAAAAAT 28% conserved"

repeat region complement(8732..8854)  
/note="L1ME repeat: matches 5436..5565 of consensus"

repeat region 8803..8817  
/note="5.0 copies 3 mer TAT 21% conserved"

repeat region 8892..8902  
/note="5.5 copies 2 mer AT 22% conserved"

repeat region 8970..9267  
/note="HAL1 repeat: matches 1507..1818 of consensus"

repeat region complement(9338..9408)  
/note="MLT1J2 repeat: matches 252..323 of consensus"

repeat region 10186..10197  
/note="2.0 copies 6 mer TTTCAC 24% conserved"

repeat region 10789..11086  
/note="AluJb repeat: matches 1..297 of consensus"

repeat region 11073..11086  
/note="14.0 copies 1 mer A 28% conserved"

repeat region 11170..11523

<u>repeat region</u>	/note="THE1B repeat: matches 1..364 of consensus" 11576..11800
<u>repeat region</u>	/note="L1MEd repeat: matches 2..249 of consensus" 11887..12242
<u>misc feature</u>	/note="L1MEd repeat: matches 363..751 of consensus" complement(11947..12544)
<u>repeat region</u>	/note="match: STS: Em:AL110056" 12237..12248
<u>repeat region</u>	/note="2.0 copies 6 mer AGTAGA 24% conserved" 12365..12537
<u>repeat region</u>	/note="L1MEd repeat: matches 904..1084 of consensus" complement(12529..13073)
<u>repeat region</u>	/note="L1MA5A repeat: matches 3652..4242 of consensus" 13076..13330
<u>repeat region</u>	/note="L1MA5A repeat: matches 4230..4483 of consensus" 13331..13638
<u>repeat region</u>	/note="AluSx repeat: matches 1..307 of consensus" 13614..13629
<u>repeat region</u>	/note="16.0 copies 1 mer A 23% conserved" 13639..15441
<u>repeat region</u>	/note="L1MA5A repeat: matches 4483..6294 of consensus" 14424..14447
<u>repeat region</u>	/note="8.0 copies 3 mer CAA 39% conserved" 14490..14500
<u>repeat region</u>	/note="2.8 copies 4 mer ACAT 22% conserved" 15063..15077
<u>repeat region</u>	/note="15.0 copies 1 mer A 30% conserved" 15091..15105
<u>repeat region</u>	/note="2.1 copies 7 mer AAGTAAA 30% conserved" 15169..15208
<u>repeat region</u>	/note="2.2 copies 18 mer GATACAAAATTACAGCTA 80% conserved" 15256..15266
<u>repeat region</u>	/note="3.7 copies 3 mer TAA 22% conserved" 15437..15453
<u>repeat region</u>	/note="2.8 copies 6 mer AAAAAT 25% conserved" 15775..15813
<u>repeat region</u>	/note="19.5 copies 2 mer TG 69% conserved" 16015..16037
<u>misc feature</u>	/note="1.9 copies 12 mer TGAGAGGCCTCT 37% conserved" complement(16370..16537)
<u>repeat region</u>	/note="match: GSS: Em:AQ044245" 16866..16878
<u>repeat region</u>	/note="2.6 copies 5 mer TTCCC 26% conserved" 17442..17817
<u>repeat region</u>	/note="LTR16C repeat: matches 85..489 of consensus" 17825..17836
<u>repeat region</u>	/note="2.4 copies 5 mer TCTTT 24% conserved" 18048..18267
<u>misc feature</u>	/note="MIR repeat: matches 12..247 of consensus" 18343..18706
<u>repeat region</u>	/note="match: GSS: Em:AQ099012" 18517..18616
<u>repeat region</u>	/note="L2 repeat: matches 2932..3031 of consensus" 18534..18544
<u>repeat region</u>	/note="3.7 copies 3 mer TTC 22% conserved" 18699..18714
<u>repeat region</u>	/note="3.2 copies 5 mer TGCAT 23% conserved" 19041..19141
<u>repeat region</u>	/note="L2 repeat: matches 3199..3312 of consensus" 19147..19156
<u>repeat region</u>	/note="2.5 copies 4 mer AAAT 20% conserved" 19309..19810
<u>repeat region</u>	/note="MLT1H repeat: matches 19..549 of consensus" 19673..19682
<u>repeat region</u>	/note="2.5 copies 4 mer CCAT 20% conserved"

repeat region 20051..20064  
/note="2.0 copies 7 mer AACAAATG 28% conserved"

repeat region 20123..20430  
/note="AluY repeat: matches 3..310 of consensus"

repeat region 20402..20418  
/note="17.0 copies 1 mer A 34% conserved"

repeat region 20416..20431  
/note="4.0 copies 4 mer AAAG 32% conserved"

repeat region 20437..20454  
/note="2.2 copies 8 mer TAGTGTGG 36% conserved"

repeat region complement(20475..20589)  
/note="L2 repeat: matches 3197..3310 of consensus"

repeat region 20658..20667  
/note="3.3 copies 3 mer ATG 20% conserved"

repeat region 20704..20714  
/note="2.2 copies 5 mer ATTGT 22% conserved"

repeat region 20893..20904  
/note="2.0 copies 6 mer TCACAA 24% conserved"

repeat region 21003..21054  
/note="MLT1H repeat: matches 107..157 of consensus"

repeat region 21187..21290  
/note="MLT1F repeat: matches 414..503 of consensus"

repeat region 21404..21570  
/note="L1MC/D repeat: matches 5265..5449 of consensus"

repeat region 21450..21460  
/note="2.8 copies 4 mer AATA 22% conserved"

repeat region 22192..22765  
/note="L1MCc repeat: matches -514..418 of consensus"

repeat region 22348..22368  
/note="2.1 copies 10 mer GGGCATCCAG 42% conserved"

repeat region 22595..22606  
/note="2.0 copies 6 mer CTGGCT 24% conserved"

repeat region 22884..23840  
/note="L1MCc repeat: matches 435..1471 of consensus"

repeat region 23773..23786  
/note="4.7 copies 3 mer AAC 28% conserved"

repeat region 23789..23798  
/note="10.0 copies 1 mer A 20% conserved"

repeat region 23841..24130  
/note="AluSc repeat: matches 1..304 of consensus"

repeat region 24106..24130  
/note="25.0 copies 1 mer A 50% conserved"

repeat region 24131..24246  
/note="L1MCc repeat: matches 1471..1579 of consensus"

repeat region 24187..24198  
/note="2.0 copies 6 mer AAGGAT 24% conserved"

repeat region 24247..24456  
/note="MSTD repeat: matches 1..213 of consensus"

repeat region 24309..24327  
/note="9.5 copies 2 mer TA 29% conserved"

repeat region 24461..25134  
/note="L1MA5 repeat: matches 4023..4699 of consensus"

repeat region 24510..24519  
/note="3.3 copies 3 mer AAG 20% conserved"

repeat region 24696..24706  
/note="2.8 copies 4 mer AATA 22% conserved"

repeat region 25135..25562  
/note="MER57B repeat: matches 1..434 of consensus"

repeat region 25563..26664  
/note="L1PA17 repeat: matches 5026..6150 of consensus"

repeat region 25642..25656  
/note="2.5 copies 6 mer CAAAAG 21% conserved"

repeat region 25957..25967  
/note="2.2 copies 5 mer CAAAA 22% conserved"

repeat region 26656..26667

<u>repeat region</u>	/note="2.4 copies 5 mer AAAAG 24% conserved" 26665..28260
<u>repeat region</u>	/note="L1MA5 repeat: matches 4697..6294 of consensus" 27145..27155
<u>repeat region</u>	/note="2.8 copies 4 mer AACC 22% conserved" 27321..27335
<u>repeat region</u>	/note="15.0 copies 1 mer A 21% conserved" 27537..27547
<u>repeat region</u>	/note="2.2 copies 5 mer AAAAC 22% conserved" 27622..27634
<u>repeat region</u>	/note="2.6 copies 5 mer AAAGG 26% conserved" 27794..27809
<u>repeat region</u>	/note="2.0 copies 8 mer ATTTCTGC 25% conserved" 27920..27937
<u>repeat region</u>	/note="3.0 copies 6 mer TAGAAG 27% conserved" 27966..27978
<u>repeat region</u>	/note="2.6 copies 5 mer AGAGG 26% conserved" 28103..28112
<u>repeat region</u>	/note="2.5 copies 4 mer AAGA 20% conserved" 28280..28413
<u>repeat region</u>	/note="MSTD repeat: matches 249..388 of consensus" 28416..28624
<u>repeat region</u>	/note="L1MCc repeat: matches 1692..1885 of consensus" 28628..28911
<u>repeat region</u>	/note="AluJo repeat: matches 1..286 of consensus" 28911..28931
<u>repeat region</u>	/note="10.5 copies 2 mer AC 33% conserved" complement(28955..29226)
<u>repeat region</u>	/note="AluJo repeat: matches 1..252 of consensus" 29016..29026
<u>repeat region</u>	/note="2.2 copies 5 mer CTCAC 22% conserved" 29094..29116
<u>repeat region</u>	/note="23.0 copies 1 mer T 28% conserved" 29245..29262
<u>repeat region</u>	/note="2.0 copies 9 mer AAGTAACAA 36% conserved" 29273..29694
<u>repeat region</u>	/note="L1MCc repeat: matches 2043..2479 of consensus" 29535..29569
<u>repeat region</u>	/note="4.4 copies 8 mer AAAAAAGC 25% conserved" complement(29928..30344)
<u>repeat region</u>	/note="MLT1L repeat: matches 110..609 of consensus" 30011..30031
<u>repeat region</u>	/note="1.9 copies 11 mer AGAGAAAGGCC 33% conserved" complement(30285..30361)
<u>repeat region</u>	/note="LTR67 repeat: matches 97..174 of consensus" 30917..30967
<u>repeat region</u>	/note="25.5 copies 2 mer TG 93% conserved" 31093..31109
<u>repeat region</u>	/note="2.1 copies 8 mer AAAGAGAT 34% conserved" complement(31180..31295)
<u>repeat region</u>	/note="MLT1K repeat: matches 111..228 of consensus" 31292..31305
<u>repeat region</u>	/note="2.0 copies 7 mer TAAAATG 28% conserved" 31429..31438
<u>repeat region</u>	/note="3.3 copies 3 mer TTC 20% conserved" 31509..31556
<u>repeat region</u>	/note="MADE1 repeat: matches 33..80 of consensus" 31669..32100
<u>repeat region</u>	/note="LTR16C repeat: matches 38..491 of consensus" 31776..31786
<u>repeat region</u>	/note="2.2 copies 5 mer AAGTC 22% conserved" 31901..31914
<u>repeat region</u>	/note="2.0 copies 7 mer TCACAGA 28% conserved" 32165..32175
<u>repeat region</u>	/note="2.2 copies 5 mer ATTTT 22% conserved"

repeat region 32453..32470  
/note="3.6 copies 5 mer AAAGA 27% conserved"

repeat region 32571..32606  
/note="2.1 copies 17 mer CAAGCTAGTAACTAAC 54% conserved"

repeat region 32790..32873  
/note="L2 repeat: matches 2922..3014 of consensus"

repeat region 32897..32955  
/note="Charlie5 repeat: matches 1..59 of consensus"

repeat region 33143..33152  
/note="2.5 copies 4 mer ATAC 20% conserved"

repeat region 33916..33929  
/note="2.0 copies 7 mer TTCCTC 28% conserved"

repeat region 34580..34591  
/note="3.0 copies 4 mer ATAA 24% conserved"

repeat region complement(34609..34923)  
/note="MLT1A repeat: matches 1..316 of consensus"

repeat region complement(34924..34993)  
/note="L1MB1 repeat: matches 6082..6152 of consensus"

repeat region 34968..34978  
/note="2.2 copies 5 mer ACAAT 22% conserved"

repeat region 34989..34999  
/note="2.2 copies 5 mer AGGCA 22% conserved"

repeat region 35137..35170  
/note="5.7 copies 6 mer TTTTTC 34% conserved"

repeat region 35150..35251  
/note="25.5 copies 4 mer TTTC 150% conserved"

repeat region 35229..35286  
/note="14.5 copies 4 mer TTCC 98% conserved"

repeat region complement(35285..35575)  
/note="AluJo repeat: matches 1..294 of consensus"

repeat region 35447..35458  
/note="12.0 copies 1 mer T 24% conserved"

repeat region 35588..35606  
/note="3.8 copies 5 mer TTTTG 31% conserved"

repeat region 35654..35665  
/note="2.0 copies 6 mer CTTATT 24% conserved"

repeat region 35729..35764  
/note="2.4 copies 15 mer CCTTCCTTCTCCCT 63% conserved"

repeat region 35767..35783  
/note="4.2 copies 4 mer CCTC 25% conserved"

repeat region complement(35820..35892)  
/note="L2 repeat: matches 3170..3243 of consensus"

repeat region 36014..36031  
/note="3.0 copies 6 mer TATTTA 27% conserved"

repeat region 36866..36882  
/note="8.5 copies 2 mer TC 34% conserved"

repeat region 37023..37077  
/note="3.7 copies 15 mer AAAATGAAATAAAAC 67% conserved"

repeat region complement(37215..37423)  
/note="MIR repeat: matches 31..261 of consensus"

repeat region 37273..37283  
/note="2.8 copies 4 mer ATTA 22% conserved"

repeat region complement(37520..37798)  
/note="L2 repeat: matches 2456..2742 of consensus"

repeat region 37766..37784  
/note="3.8 copies 5 mer GGAGG 29% conserved"

repeat region 37896..37906  
/note="2.8 copies 4 mer AAAG 22% conserved"

repeat region 37954..37965  
/note="12.0 copies 1 mer A 24% conserved"

repeat region complement(38128..38424)  
/note="AluSg repeat: matches 2..297 of consensus"

repeat region 38128..38144  
/note="17.0 copies 1 mer T 34% conserved"

repeat region 38492..38911

<u>repeat region</u>	/note="MER63B repeat: matches 1..435 of consensus" 38494..38504
<u>repeat region</u>	/note="2.2 copies 5 mer GTGAT 22% conserved" complement(38945..39370)
<u>repeat region</u>	/note="MER57A repeat: matches 1..403 of consensus" 38967..38976
<u>repeat region</u>	/note="2.0 copies 5 mer AAATT 20% conserved" complement(39472..39532)
<u>repeat region</u>	/note="L2 repeat: matches 3205..3262 of consensus" complement(39534..39674)
<u>repeat region</u>	/note="MIR repeat: matches 108..259 of consensus" 39631..39640
<u>repeat region</u>	/note="3.3 copies 3 mer TAT 20% conserved" 39720..39729
<u>repeat region</u>	/note="2.5 copies 4 mer ATAA 20% conserved" 39931..39964
<u>repeat region</u>	/note="2.1 copies 16 mer ATGGATAAATAAATTA 59% conserved" 39935..39944
<u>repeat region</u>	/note="2.5 copies 4 mer ATAA 20% conserved" 39954..39967
<u>repeat region</u>	/note="3.5 copies 4 mer AATT 28% conserved" 40707..41300
<u>misc feature</u>	/note="match: GSS: Em:AG040344"
<u>repeat region</u>	40893..40925
<u>repeat region</u>	/note="16.5 copies 2 mer TA 41% conserved" complement(40925..41068)
<u>repeat region</u>	/note="AluSg/x repeat: matches 145..288 of consensus" 41444..41755
<u>repeat region</u>	/note="L2 repeat: matches 2697..3050 of consensus" complement(41764..42122)
<u>repeat region</u>	/note="MLT1A repeat: matches 21..365 of consensus" 41860..41871
<u>repeat region</u>	/note="2.0 copies 6 mer TCAAGA 24% conserved" complement(42157..42433)
<u>repeat region</u>	/note="LTR16C repeat: matches 88..391 of consensus" 42162..42175
<u>repeat region</u>	/note="2.3 copies 6 mer AGTGAG 28% conserved" 42759..42771
<u>repeat region</u>	/note="2.2 copies 6 mer ATTTTA 26% conserved" complement(42785..42863)
<u>repeat region</u>	/note="MLT1J2 repeat: matches 368..448 of consensus" 42864..42880
<u>repeat region</u>	/note="2.1 copies 8 mer AAAATAAT 34% conserved" 42866..42885
<u>repeat region</u>	/note="6.7 copies 3 mer AAT 24% conserved" complement(42894..43239)
<u>repeat region</u>	/note="MLT1J2 repeat: matches 23..386 of consensus" 43074..43099
<u>repeat region</u>	/note="6.5 copies 4 mer AGAA 25% conserved" 43258..43274
<u>repeat region</u>	/note="2.4 copies 7 mer AAATTAG 25% conserved" complement(43270..43331)
<u>repeat region</u>	/note="MER113 repeat: matches 32..95 of consensus" 43285..43294
<u>repeat region</u>	/note="3.3 copies 3 mer TAA 20% conserved" 43413..43703
<u>misc feature</u>	/note="match: GSS: Em:AQ015991"
<u>repeat region</u>	complement(43476..43514)
<u>repeat region</u>	/note="MLT1H repeat: matches 538..577 of consensus" complement(43521..43739)
<u>repeat region</u>	/note="MLT1H repeat: matches 133..375 of consensus" 43708..43724
<u>repeat region</u>	/note="2.4 copies 7 mer CCACAAG 25% conserved" complement(43740..44231)
<u>repeat region</u>	/note="MLT2B2 repeat: matches 1..515 of consensus"



repeat region 43777..43811  
/note="3.5 copies 10 mer AGACATAGAT 34% conserved"

repeat region 43787..43799  
/note="3.2 copies 4 mer ATAG 26% conserved"

repeat region 43805..43829  
/note="4.2 copies 6 mer ACAGAC 41% conserved"

repeat region 44002..44012  
/note="2.8 copies 4 mer TCAA 22% conserved"

repeat region 44352..44361  
/note="10.0 copies 1 mer A 20% conserved"

misc feature complement(44542..44977)  
/note="match: GSS: Em:AQ358298"

repeat region 44830..45320  
/note="MLT1H repeat: matches 1..549 of consensus"

repeat region 45523..45540  
/note="2.2 copies 8 mer AAACATGA 27% conserved"

repeat region 45570..45674  
/note="MLT1J2 repeat: matches 325..428 of consensus"

repeat region 45791..45806  
/note="2.3 copies 7 mer ATTGATT 23% conserved"

misc feature 45853..46320  
/note="match: GSS: Em:AQ186434"

repeat region complement(46233..46722)  
/note="L1ME3 repeat: matches 5657..6158 of consensus"

repeat region 46777..46875  
/note="L1ME3A repeat: matches 5743..5846 of consensus"

repeat region 46990..47021  
/note="16.0 copies 2 mer GT 64% conserved"

repeat region 47140..47154  
/note="5.0 copies 3 mer ATA 21% conserved"

repeat region 47427..47443  
/note="2.4 copies 7 mer AGGAGAA 25% conserved"

repeat region 48160..48233  
/note="MER58 repeat: matches 25..98 of consensus"

repeat region 48223..48253  
/note="2.1 copies 15 mer TTTTAAATGGTCATA 44% conserved"

repeat region 48247..48348  
/note="MER58 repeat: matches 2318..2417 of consensus"

repeat region 48457..48560  
/note="MLT1J2 repeat: matches 32..133 of consensus"

repeat region 48655..48816  
/note="MLT1J2 repeat: matches 288..450 of consensus"

repeat region 48880..48894  
/note="7.5 copies 2 mer AC 30% conserved"

repeat region 50127..50602  
/note="L1MC4 repeat: matches 7392..7858 of consensus"

repeat region 50173..50182  
/note="2.0 copies 5 mer AACAT 20% conserved"

repeat region 50243..50255  
/note="2.2 copies 6 mer ATACAA 26% conserved"

repeat region 50380..50393  
/note="2.3 copies 6 mer ATGACA 28% conserved"

repeat region complement(50622..50888)  
/note="MLT1H repeat: matches 224..531 of consensus"

repeat region 50893..50936  
/note="22.0 copies 2 mer CA 88% conserved"

repeat region 50936..50998  
/note="31.5 copies 2 mer AG 72% conserved"

repeat region complement(50977..51089)  
/note="MLT1H repeat: matches 90..231 of consensus"

repeat region 51256..51413  
/note="L1ME3A repeat: matches 5876..6065 of consensus"

repeat region 51508..51657  
/note="MIR3 repeat: matches 23..179 of consensus"

repeat region complement(52443..52527)

repeat region /note="L2 repeat: matches 3204..3312 of consensus"  
52443..52452

repeat region /note="2.5 copies 4 mer TTCA 20% conserved"  
complement(52602..52691)

repeat region /note="MIR repeat: matches 101..187 of consensus"  
52649..52666

repeat region /note="2.0 copies 9 mer CAGACGAGG 27% conserved"  
52772..52984

repeat region /note="MER58A repeat: matches 1..223 of consensus"  
complement(53007..53400)

repeat region /note="MLT1J2 repeat: matches 1..445 of consensus"  
53222..53232

repeat region /note="2.2 copies 5 mer AAAAG 22% conserved"  
53515..53738

repeat region /note="L1MC5 repeat: matches 7701..7928 of consensus"  
53789..53812

repeat region /note="4.8 copies 5 mer AAAAT 32% conserved"  
complement(54168..54323)

repeat region /note="MLT1J2 repeat: matches 267..434 of consensus"  
54341..54661

repeat region /note="AluSx repeat: matches 1..312 of consensus"  
54620..54632

repeat region /note="13.0 copies 1 mer A 26% conserved"  
54633..54647

repeat region /note="3.8 copies 4 mer GAAT 30% conserved"  
54646..54661

repeat region /note="16.0 copies 1 mer A 23% conserved"  
55244..55258

repeat region /note="3.8 copies 4 mer ATTC 21% conserved"  
55249..55270

repeat region /note="1.8 copies 12 mer TTCATACATTTG 37% conserved"  
55694..55705

repeat region /note="2.0 copies 6 mer CCCTTT 24% conserved"  
56046..56055

repeat region /note="2.5 copies 4 mer AGTT 20% conserved"  
56363..56373

repeat region /note="2.8 copies 4 mer TTAT 22% conserved"  
56397..58342

misc feature /note="CpG island"  
/evidence=not\_experimental

repeat region 56508..56526

repeat region /note="3.8 copies 5 mer GGGCT 20% conserved"  
57013..57027

repeat region /note="3.0 copies 5 mer CTCCC 21% conserved"  
57209..57220

repeat region /note="2.0 copies 6 mer CTCCAG 24% conserved"  
57255..57269

repeat region /note="3.0 copies 5 mer CCACC 23% conserved"  
57259..57271

repeat region /note="3.2 copies 4 mer CCCA 26% conserved"  
57458..57472

repeat region /note="3.0 copies 5 mer GCGGC 21% conserved"  
57534..57549

repeat region /note="2.7 copies 6 mer GGCGAG 23% conserved"  
57541..57654

misc feature /note="Single clone region. single clone region containing  
only reads from a Short insert library of 20bae55h7.  
Assembly consistant with digest."

repeat region 57586..57659

repeat region /note="24.7 copies 3 mer CCT 121% conserved"  
57677..57689

repeat region /note="2.2 copies 6 mer CCGCTC 26% conserved"  
57699..58288

repeat region /note="L1M2 repeat: matches 661..1268 of consensus"  
57748..57769

repeat region /note="4.4 copies 5 mer CCCGC 26% conserved"  
57749..57762

repeat region /note="4.7 copies 3 mer CCG 21% conserved"  
57794..57807

repeat region /note="2.8 copies 5 mer CCGGC 28% conserved"  
57831..57843

repeat region /note="2.2 copies 6 mer GTCTCC 26% conserved"  
57841..57857

repeat region /note="5.7 copies 3 mer CCG 34% conserved"  
57926..57954

repeat region /note="9.7 copies 3 mer GCG 49% conserved"  
58021..58050

repeat region /note="2.5 copies 12 mer GGAGCCCAGGCG 42% conserved"  
58057..58073

repeat region /note="2.1 copies 8 mer CCGGGCTC 34% conserved"  
58070..58085

repeat region /note="5.3 copies 3 mer CTC 23% conserved"  
58096..58122

repeat region /note="9.0 copies 3 mer CCG 38% conserved"  
58098..58122

repeat region /note="3.6 copies 7 mer GCCGCCG 34% conserved"  
58170..58199

repeat region /note="10.0 copies 3 mer GCT 42% conserved"  
58238..58257

repeat region /note="2.0 copies 10 mer CCGACGCGGC 33% conserved"  
58518..58527

repeat region /note="2.5 copies 4 mer TCTG 20% conserved"  
58603..58612

repeat region /note="2.5 copies 4 mer TGCT 20% conserved"  
58836..58847

repeat region /note="2.0 copies 6 mer TTCCTC 24% conserved"  
59256..59559

repeat region /note="AluSx repeat: matches 3..312 of consensus"  
59530..59564

repeat region /note="35.0 copies 1 mer A 25% conserved"  
59531..59593

repeat region /note="12.6 copies 5 mer AAAAT 80% conserved"  
59646..59664

repeat region /note="1.9 copies 10 mer CTTTATACAT 29% conserved"  
complement(59700..59873)

repeat region /note="MIR repeat: matches 82..260 of consensus"  
60390..60614

misc feature /note="match: GSS: Em:AQ046228  
match: STS: Em:G50471"

repeat region 60507..60518

repeat region /note="2.0 copies 6 mer CAGCTT 24% conserved"  
60828..60837

repeat region /note="2.5 copies 4 mer TTCT 20% conserved"  
61115..61124

repeat region /note="3.3 copies 3 mer AGT 20% conserved"  
complement(61136..61206)

repeat region /note="MIR repeat: matches 193..262 of consensus"  
61206..61217

repeat region /note="3.0 copies 4 mer CTTT 24% conserved"  
complement(61207..61525)

repeat region /note="AluY repeat: matches 1..311 of consensus"  
61215..61236

repeat region /note="22.0 copies 1 mer T 44% conserved"  
61386..61399

repeat region /note="14.0 copies 1 mer T 28% conserved"  
complement(61526..61637)

repeat region /note="MIR repeat: matches 77..193 of consensus"  
61798..61812

repeat region /note="7.5 copies 2 mer AT 21% conserved"  
62222..62233

repeat region /note="2.0 copies 6 mer TTAATG 24% conserved"  
62245..62271

repeat region /note="4.5 copies 6 mer ATAGAT 45% conserved"  
62788..62798

repeat region /note="11.0 copies 1 mer T 22% conserved"  
complement(62812..63323)

repeat region /note="MLT1H repeat: matches 18..549 of consensus"  
complement(63386..63567)

repeat region /note="L1M4 repeat: matches 2247..2434 of consensus"  
complement(63587..63875)

repeat region /note="AluY repeat: matches 1..289 of consensus"  
63591..64190

repeat region /note="15.0 copies 40 mer  
TTTTGAGACGGAGTCTCACTCTATACCCAGGCTGGAGTG 909% conserved"  
complement(63880..64180)

repeat region /note="AluY repeat: matches 1..301 of consensus"  
63880..63899

repeat region /note="20.0 copies 1 mer T 31% conserved"  
64188..64197

repeat region /note="2.0 copies 5 mer TTAA 20% conserved"  
64321..64331

repeat region /note="3.7 copies 3 mer GCT 22% conserved"  
complement(64333..64645)

repeat region /note="AluSx repeat: matches 1..305 of consensus"  
64333..64355

repeat region /note="23.0 copies 1 mer T 37% conserved"  
64645..64658

repeat region /note="4.7 copies 3 mer CTG 28% conserved"  
complement(64676..65154)

repeat region /note="HAL1 repeat: matches 1214..1726 of consensus"  
64852..64861

repeat region /note="2.0 copies 5 mer AATTT 20% conserved"  
65434..65470

repeat region /note="3.4 copies 11 mer CTTTTCTTTC 51% conserved"  
65446..65528

repeat region /note="20.8 copies 4 mer CTTT 37% conserved"  
65475..65487

repeat region /note="2.6 copies 5 mer TTCCT 26% conserved"  
65505..65524

repeat region /note="10.0 copies 2 mer TC 33% conserved"  
65532..65550

repeat region /note="1.9 copies 10 mer TTTTTTAAAG 38% conserved"  
complement(65542..66060)

repeat region /note="L1ME2 repeat: matches 5634..6164 of consensus"  
66207..66216

repeat region /note="5.0 copies 2 mer CT 20% conserved"  
complement(66506..66872)

repeat region /note="L3b repeat: matches 1114..1476 of consensus"  
66655..66673

repeat region /note="2.1 copies 9 mer TGTTCACTT 38% conserved"  
66945..66955

repeat region /note="2.2 copies 5 mer AAAGA 22% conserved"  
67043..67053

repeat region /note="2.2 copies 5 mer GATGG 22% conserved"  
67091..67100

repeat region /note="2.5 copies 4 mer CAAA 20% conserved"  
67118..67147

repeat region /note="6.0 copies 5 mer AGAAA 44% conserved"  
67120..67148

repeat region /note="29.0 copies 1 mer A 31% conserved"  
67189..67206

repeat region /note="2.0 copies 9 mer TTATAAGAA 36% conserved"  
67235..67247

repeat region /note="3.2 copies 4 mer TTTC 26% conserved"  
67311..67498

<u>repeat region</u>	/note="LTR16C repeat: matches 289..488 of consensus" 67609..67618
<u>repeat region</u>	/note="3.3 copies 3 mer TTG 20% conserved" 68515..68525
<u>repeat region</u>	/note="3.7 copies 3 mer TTA 22% conserved" complement(68524..68539)
<u>repeat region</u>	/note="L1MA10 repeat: matches 6319..6334 of consensus" complement(68540..69072)
<u>repeat region</u>	/note="L1ME1 repeat: matches 5582..6161 of consensus" 68776..68790
<u>repeat region</u>	/note="3.0 copies 5 mer TGCAT 21% conserved" 68816..68825
<u>repeat region</u>	/note="2.5 copies 4 mer ATTC 20% conserved" 69398..69414
<u>repeat region</u>	/note="17.0 copies 1 mer A 25% conserved" 69473..69489
<u>repeat region</u>	/note="1.9 copies 9 mer ATTCTCTTG 27% conserved" 69481..69508
<u>repeat region</u>	/note="2.2 copies 13 mer ATTCTCTTGCCCC 40% conserved" 69688..69987
<u>repeat region</u>	/note="AluSp repeat: matches 2..302 of consensus" 69969..69987
<u>repeat region</u>	/note="19.0 copies 1 mer A 38% conserved" 70233..70333
<u>repeat region</u>	/note="MER5A repeat: matches 9..112 of consensus" complement(70347..71285)
<u>repeat region</u>	/note="L1PB4 repeat: matches 5215..6152 of consensus" 70594..70605
<u>repeat region</u>	/note="2.0 copies 6 mer TTTCTG 24% conserved" 71051..71065
<u>repeat region</u>	/note="2.5 copies 6 mer TTTTAA 21% conserved" 71104..71128
<u>repeat region</u>	/note="2.3 copies 11 mer TTGTTGTCCTC 32% conserved" 71286..71350
<u>repeat region</u>	/note="MER5A repeat: matches 124..189 of consensus" 71430..71439
<u>repeat region</u>	/note="3.3 copies 3 mer TAA 20% conserved" 71501..71516
<u>repeat region</u>	/note="2.0 copies 8 mer CATGGGTC 32% conserved" complement(71650..71724)
<u>repeat region</u>	/note="MLT1I repeat: matches 104..180 of consensus" 71726..71873
<u>repeat region</u>	/note="MIR repeat: matches 25..183 of consensus" 72208..72223
<u>repeat region</u>	/note="4.0 copies 4 mer TTCC 23% conserved" complement(72301..72592)
<u>repeat region</u>	/note="AluSc repeat: matches 4..294 of consensus" 72301..72315
<u>repeat region</u>	/note="15.0 copies 1 mer T 21% conserved" 72378..72389
<u>repeat region</u>	/note="2.0 copies 6 mer ACCTCC 24% conserved" 72445..72454
<u>repeat region</u>	/note="3.3 copies 3 mer CCA 20% conserved" complement(72715..72839)
<u>repeat region</u>	/note="THE1A repeat: matches 1..126 of consensus" complement(72840..73499)
<u>repeat region</u>	/note="THE1A-int repeat: matches 918..1580 of consensus" 72941..72960
<u>repeat region</u>	/note="2.9 copies 7 mer AAAGTCC 31% conserved" 73481..73492
<u>repeat region</u>	/note="2.0 copies 6 mer CCCTGC 24% conserved" complement(73505..73581)
<u>repeat region</u>	/note="THE1A repeat: matches 1..80 of consensus" 73583..74087
<u>repeat region</u>	/note="L1ME3A repeat: matches 5610..6157 of consensus"

gene complement(join(74174..74482,75357..75477,75826..76047))  
/gene="dJ1077I2.4"  
mRNA complement(join(74174..74482,75357..75477,75826..76047))  
/gene="dJ1077I2.4"  
/product="dJ1077I2.4 (Putative novel transcript)"  
/note="match: ESTs: Em:BI463885"  
/evidence=not\_experimental  
repeat region 74749..74764  
/note="2.0 copies 8 mer GGCAAAAT 32% conserved"  
repeat region 75388..75401  
/note="2.0 copies 7 mer AGTGTGA 28% conserved"  
repeat region 75754..75766  
/note="2.2 copies 6 mer TGGCCT 26% conserved"  
repeat region 75818..75827  
/note="2.5 copies 4 mer TTAC 20% conserved"  
repeat region 76136..76145  
/note="2.0 copies 5 mer TCATT 20% conserved"  
repeat region 76515..76528  
/note="3.5 copies 4 mer CATT 28% conserved"  
repeat region complement(76516..77245)  
/note="L2 repeat: matches 2448..3313 of consensus"  
repeat region 77144..77153  
/note="2.5 copies 4 mer TGGA 20% conserved"  
repeat region complement(77281..77325)  
/note="L2 repeat: matches 2304..2348 of consensus"  
repeat region complement(77352..78690)  
/note="L2 repeat: matches 586..2082 of consensus"  
repeat region 78727..78736  
/note="2.5 copies 4 mer TTTG 20% conserved"  
repeat region 78739..78756  
/note="3.0 copies 6 mer GTTTTT 27% conserved"  
repeat region complement(79263..79475)  
/note="MIR repeat: matches 10..241 of consensus"  
repeat region 79532..79626  
/note="MIR repeat: matches 34..130 of consensus"  
repeat region complement(79628..79686)  
/note="MLT1J1 repeat: matches 265..326 of consensus"  
repeat region complement(79699..79732)  
/note="MLT1I repeat: matches 127..160 of consensus"  
gene complement(join(80437..80754,81615..81742))  
/gene="dJ1077I2.3"  
mRNA complement(join(80437..80754,81615..81742))  
/gene="dJ1077I2.3"  
/product="dJ1077I2.3 (Putative novel transcript)"  
/note="match: ESTs: Em:BF510052"  
/evidence=not\_experimental  
polyA site complement(80439)  
/gene="dJ1077I2.3"  
repeat region 80508..80518  
/note="2.8 copies 4 mer ACAG 22% conserved"  
repeat region 80761..80774  
/note="14.0 copies 1 mer A 28% conserved"  
repeat region 81478..81489  
/note="3.0 copies 4 mer CTTC 24% conserved"  
repeat region complement(81491..81658)  
/note="MLT1E repeat: matches 439..593 of consensus"  
repeat region complement(81652..81945)  
/note="MLT1E repeat: matches 1..303 of consensus"  
repeat region 82056..82073  
/note="3.6 copies 5 mer TTCAT 27% conserved"  
repeat region 82067..82082  
/note="2.3 copies 7 mer TCATTTC 32% conserved"  
repeat region 82072..82089  
/note="2.0 copies 9 mer TCTCATTTC 27% conserved"  
repeat region 82359..82660

repeat region /note="AluSx repeat: matches 1..297 of consensus"  
82646..82660  
/note="15.0 copies 1 mer A 30% conserved"  
repeat region complement(82983..83071)  
/note="MIR repeat: matches 47..144 of consensus"  
repeat region 83149..83158  
/note="2.0 copies 5 mer CTTTT 20% conserved"  
repeat region 83257..83266  
/note="10.0 copies 1 mer T 20% conserved"  
repeat region 83311..83325  
/note="7.5 copies 2 mer AT 21% conserved"  
repeat region 83328..83621  
/note="AluSq repeat: matches 2..299 of consensus"  
repeat region 83606..83615  
/note="10.0 copies 1 mer A 20% conserved"  
repeat region 83891..83932  
/note="21.0 copies 2 mer GT 84% conserved"  
repeat region 83931..83943  
/note="3.2 copies 4 mer GTAG 26% conserved"  
repeat region 84233..84247  
/note="7.5 copies 2 mer GT 21% conserved"  
repeat region 84562..84573  
/note="2.0 copies 6 mer TATTCT 24% conserved"  
repeat region 85418..85429  
/note="2.4 copies 5 mer GGTC A 24% conserved"  
repeat region 85511..85521  
/note="2.2 copies 5 mer AAATA 22% conserved"  
repeat region 86153..86211  
/note="11.8 copies 5 mer GTTTT 118% conserved"  
repeat region 86312..86322  
/note="2.2 copies 5 mer TAATG 22% conserved"  
repeat region complement(86895..87015)  
/note="MER5B repeat: matches 54..172 of consensus"  
repeat region 87029..87150  
/note="L2 repeat: matches 3144..3272 of consensus"  
repeat region 87464..87474  
/note="2.8 copies 4 mer CCTC 22% conserved"  
repeat region 87614..87624  
/note="2.2 copies 5 mer TTCCA 22% conserved"  
misc feature 87870..88316  
/note="match: GSS: Em:AQ457776"  
repeat region 88004..88016  
/note="2.2 copies 6 mer AGCTAG 26% conserved"  
repeat region 88039..88048  
/note="2.5 copies 4 mer AGCA 20% conserved"  
repeat region 88332..88345  
/note="3.5 copies 4 mer AAGC 28% conserved"  
repeat region 88590..88599  
/note="2.5 copies 4 mer TGAA 20% conserved"  
repeat region 88730..88741  
/note="2.0 copies 6 mer AAAAGT 24% conserved"  
repeat region 88842..89139  
/note="AluSx repeat: matches 1..293 of consensus"  
repeat region 88962..88978  
/note="2.1 copies 8 mer AAAAATAC 34% conserved"  
repeat region 89129..89139  
/note="11.0 copies 1 mer A 22% conserved"  
repeat region complement(89924..90101)  
/note="MER5A repeat: matches 6..189 of consensus"  
repeat region 90107..90117  
/note="2.2 copies 5 mer AATTA 22% conserved"  
repeat region 90203..90214  
/note="2.0 copies 6 mer TAAAAT 24% conserved"  
repeat region 90216..90227  
/note="2.0 copies 6 mer ACACAT 24% conserved"

repeat region 90226..90239  
/note="2.3 copies 6 mer ATCCAT 28% conserved"

repeat region 90236..90251  
/note="8.0 copies 2 mer AT 32% conserved"

repeat region 90251..90261  
/note="5.5 copies 2 mer TG 22% conserved"

repeat region 90309..90630  
/note="AluSx repeat: matches 1..307 of consensus"

repeat region 90432..90452  
/note="21.0 copies 1 mer A 42% conserved"

repeat region 90608..90630  
/note="5.8 copies 4 mer AAAT 46% conserved"

repeat region 90655..90675  
/note="10.5 copies 2 mer AT 24% conserved"

repeat region 90658..90674  
/note="2.8 copies 6 mer TATATT 34% conserved"

repeat region 90678..90690  
/note="2.2 copies 6 mer CATATA 26% conserved"

repeat region 90794..90806  
/note="2.2 copies 6 mer TCAGAA 26% conserved"

repeat region 91258..91267  
/note="2.5 copies 4 mer TTCC 20% conserved"

repeat region complement(91289..91616)  
/note="L2 repeat: matches 2982..3312 of consensus"

repeat region 91291..91300  
/note="2.5 copies 4 mer CATT 20% conserved"

repeat region 91549..91558  
/note="5.0 copies 2 mer CT 20% conserved"

repeat region 91758..91768  
/note="5.5 copies 2 mer TG 22% conserved"

repeat region 91819..91830  
/note="2.4 copies 5 mer AAAAG 24% conserved"

repeat region complement(91840..91994)  
/note="L2 repeat: matches 2945..3108 of consensus"

repeat region complement(92094..92166)  
/note="MER91A repeat: matches 8..82 of consensus"

repeat region 92259..92272  
/note="3.5 copies 4 mer CATT 28% conserved"

repeat region 92299..92309  
/note="11.0 copies 1 mer T 22% conserved"

repeat region 92487..92791  
/note="AluSx repeat: matches 1..305 of consensus"

repeat region 92695..92706  
/note="2.0 copies 6 mer GGAGGT 24% conserved"

repeat region 92769..92791  
/note="23.0 copies 1 mer A 46% conserved"

repeat region 92910..92927  
/note="2.2 copies 8 mer GGGATCAT 36% conserved"

repeat region 93142..93196  
/note="MIR repeat: matches 113..163 of consensus"

repeat region 93281..93298  
/note="2.0 copies 9 mer AGGTGGAGG 36% conserved"

repeat region 93288..93300  
/note="2.2 copies 6 mer GGAGGT 26% conserved"

repeat region 93398..93408  
/note="2.2 copies 5 mer AGAGA 22% conserved"

repeat region complement(93452..93501)  
/note="MIR repeat: matches 91..144 of consensus"

repeat region 93557..93568  
/note="2.4 copies 5 mer AAAAT 24% conserved"

repeat region 93566..93577  
/note="2.0 copies 6 mer TAACAG 24% conserved"

repeat region 93606..93832  
/note="AluSq repeat: matches 1..225 of consensus"

repeat region 93751..93760



repeat region /note="3.3 copies 3 mer GTG 20% conserved"  
94085..94098

repeat region /note="14.0 copies 1 mer A 28% conserved"  
94355..94452

repeat region /note="MIR repeat: matches 111..219 of consensus"  
94503..94647

repeat region /note="LTR33 repeat: matches 14..160 of consensus"  
94674..94898

repeat region /note="LTR33 repeat: matches 301..521 of consensus"  
95374..95677

repeat region /note="AluSx repeat: matches 1..306 of consensus"  
95654..95677

repeat region /note="24.0 copies 1 mer A 30% conserved"  
complement(95813..96278)

repeat region /note="LTR37B repeat: matches 1..468 of consensus"  
95893..95902

repeat region /note="2.5 copies 4 mer AATG 20% conserved"  
95972..95981

repeat region /note="3.3 copies 3 mer ATG 20% conserved"  
96295..96360

repeat region /note="L2 repeat: matches 3198..3268 of consensus"  
96404..96415

repeat region /note="2.4 copies 5 mer AGCTA 24% conserved"  
96976..96989

repeat region /note="14.0 copies 1 mer T 28% conserved"  
complement(97136..97231)

repeat region /note="MLT1H repeat: matches 453..549 of consensus"  
complement(97339..97441)

repeat region /note="MLT1H repeat: matches 197..305 of consensus"  
97505..97822

repeat region /note="AluSq repeat: matches 1..307 of consensus"  
97582..98164

misc feature /note="match: GSS: Em:AQ318861"  
97649..97661

repeat region /note="4.3 copies 3 mer GTG 26% conserved"  
97799..97819

repeat region /note="21.0 copies 1 mer A 33% conserved"  
complement(97917..98012)

repeat region /note="MIR repeat: matches 17..113 of consensus"  
97968..97983

repeat region /note="2.7 copies 6 mer GACCCA 32% conserved"  
98280..98295

repeat region /note="2.7 copies 6 mer GCCTGG 23% conserved"  
98622..98640

repeat region /note="1.9 copies 10 mer CTGGTGGCCA 38% conserved"  
98636..98646

repeat region /note="2.2 copies 5 mer TGGCC 22% conserved"  
98827..98849

repeat region /note="23.0 copies 1 mer T 28% conserved"  
complement(98879..99267)

misc feature /note="match: GSS: Em:AQ630216"  
99384..99798

misc feature /note="match: GSS: Em:AQ718436"  
99746..99755

repeat region /note="2.5 copies 4 mer TCCA 20% conserved"  
100252..100265

repeat region /note="2.0 copies 7 mer TGTGTGTT 28% conserved"  
100409..100419

repeat region /note="2.2 copies 5 mer TAAAA 22% conserved"  
100973..100999

repeat region /note="3.0 copies 9 mer ACTCTGACC 36% conserved"  
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repeat region /note="3.0 copies 4 mer CTTT 24% conserved"  
complement(101824..102026)

repeat region /note="L1MC4 repeat: matches 6797..7002 of consensus"

repeat region 102051..102103  
 /note="MADE1 repeat: matches 1..53 of consensus"  
repeat region 102189..102204  
 /note="2.7 copies 6 mer TTAACA 23% conserved"  
repeat region complement(102213..102624)  
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misc feature complement(102530..103055)  
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misc feature 103056..103395  
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 /note="4.0 copies 4 mer ATCA 32% conserved"  
repeat region 104165..104175  
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repeat region 104471..104777  
 /note="153.5 copies 2 mer CT 150% conserved"  
repeat region 104488..104776  
 /note="57.8 copies 5 mer TCTTC 240% conserved"  
repeat region 104660..104720  
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 /note="3.0 copies 4 mer TTAT 24% conserved"  
repeat region 106283..106347  
 /note="16.2 copies 4 mer TGGA 78% conserved"  
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